Erratum

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MicroRNAs in plants

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As a result of a Printer error, the sequence of MIR168 was printed incorrectly in Table 1. The cloning frequencies of MIR163 and MIR164 were also incorrectly reported. Both were cloned twice. The correct table is printed below, along with its legend.

Supplemental material for this article is now available online at http://www.genesdev.org.

The authors apologize for any inconvenience this may have caused.

Table 1. *MicroRNAs cloned from* Arabidopsis

miRNA gene	No. of clones	miRNA sequence	miRNA length (nt)	*Oryza* matches	Fold-back arm	Fold-back length	Chr.	Distance to nearest gene
MIR156a	16	UGACAGAAGAGAGUGAGCAC	20–21	10	5′	82	2	3.2 kb downstream of At2g25100 (s)
MIR156b					5′	80	4	0.36 kb upstream of At4g30970 (a)
MIR156c					5′	83	4	3.2 kb downstream of At4g31875 (s)
MIR156d					5′	86	5	2.6 kb upstream of At5g10940 (s)
MIR156e					5′	96	5	1.6 kb downstream of At5g11980 (s)
MIR156f					5′	90	5	1.3 kb downstream of At5g26150 (a)
MIR157a	9	UUGACAGAAGAUAGAGAGCAC	20–21	—	5′	91	1	1.8 kb downstream of At1g66780 (a)
MIR157b					5′	91	1	2.7 kb downstream of At1g66790 (a)
MIR157c					5′	165	3	2.3 kb downstream of At3g18215 (a)
MIR157d					5′	173	1	1.0 kb upstream of At1g48470 (s)
MIR158	8	UCCCAAAUGUAGACAAAGCA	20	—	3′	64	3	0.6 kb upstream of At3g10750 (s)
MIR159	8	UUUGGAUUGAAGGGAGCUCUA	21	—	3′	182	1	1.9 kb upstream of At1g73690 (s)
MIR160a	4	UGCCUGGCUCCCUGUAUGCCA	21	4	5′	78	2	4.0 kb downstream of At2g39180 (a)
MIR160b					5′	80	4	2.4 kb upstream of At4g17790 (a)
MIR160c					5′	81	5	1.5 kb upstream of At5g46850 (a)
MIR161	16	UUGAAAGUGACUACAUCGGGG	20–21	—	5′	90	1	2.6 kb downstream of At1g48270 (a)
MIR162a	3	UCGAUAAACCUCUGCAUCCAG	21	1	3′	85	5	1.2 kb upstream of At5g08190 (s)
MIR162b					3′	88	5	1.4 kb upstream of At5g23070 (s)
MIR163	2	UUGAAGAGGACUUGGAACUUCGAU	24	—	3′	303	1	0.6 kb upstream of At1g66730 (s)
MIR164a	2	UGGAGAAGCAGGGCACGUGCA	21	2	5′	78	2	1.1 kb upstream of At2g47590 (s)
MIR164b					5′	149	5	2.4 kb upstream of At5g01750 (s)
MIR165a	2	UCGGACCAGGCUUCAUCCCCC	20–21	—	3′	101	1	1.5 kb downstream of At1g01180 (a)
MIR165b					3′	136	4	2.8 kb upstream of At4g00880 (s)
MIR166a	5	UCGGACCAGGCUUCAUUCCCC	21	6	3′	136	2	4.7 kb upstream of At2g46690 (a)
MIR166b					3′	112	3	3.5 kb upstream of At3g61900 (a)
MIR166c					3′	108	5	10 kb downstream of At5g08690 (s)
MIR166d					3′	101	5	22 kb downstream of At5g08740 (a)
MIR166e					3′	135	5	2.6 kb downstream of At5g41910 (a)
MIR166f					3′	91	5	1.1 kb downstream of At5g43600 (s)
MIR166g					3′	90	5	1.5 kb upstream of At5g63720 (s)
MIR167a	19	UGAAGCUGCCAGCAUGAUCUA	21	3	5′	101	3	4.7 kb upstream of At3g22890 (a)
MIR167b					5′	90	3	0.19 kb downstream of At3g63370 (s)
MIR168a	3	UCGCUUGGUGCAGGUCGGGAA	21	—	5′	104	4	2.3 kb upstream of At4g19390 (a)
MIR168b					5′	89	5	0.5 kb downstream of At5g45310 (s)
MIR169	3	CAGCCAAGGAUGACUUGCCGA	21	2[a]	5′	190	3	1.9 kb downstream of At3g13400 (a)
MIR170	3	UGAUUGAGCCGUGUCAAUAUC	21	—	3′	64	5	0.5 kb downstream of At5g66040 (s)
MIR171	10	UGAUUGAGCCGCGCCAAUAUC	21	5[b]	3′	92	3	0.5 kb downstream of At3g51380 (a)
					—	—	2	in At2g45160 SCARECROW-like (a)
					—	—	3	in At3g60630 SCARECROW-like (a)
					—	—	4	in At4g00150 SCARECROW-like 6 (a)

Some miRNAs are represented by clones of different lengths due to heterogeneity of the RNA ends. The sequence of the most abundant clone is shown. Both miR156 and miR161 clones were found with 5′ or 3′ heterogeneity. *MIR160nb* and *MIR161* each had one clone of the same size but in a register shifted 5′ of the sequence shown by 2 and 8 nucleotides, respectively. The number of perfect matches to the available rice genomic sequence (*Oryza* matches) are indicated, as is the arm of the predicted stem-loop precursor that contains the miRNA (Fold-back arm) and the minimum number of nt that would be required to from a fold-back structure bounded by the miRNA and the segment of the predicted precursor that pairs to the miRNA (Fold-back length). *Oryza* fold-backs have the miRNA in the same arm as their *Arabidopsis* homologs (Supplemental data available online at http://www. genesdev.org). Chromosomal (Chr) positions, distance to the nearest annotated gene, and the position of the miRNA, sense (s) and antisense (a), relative to the nearest gene are noted for all matches in the *Arabidopsis* genome.
[a]One of the miR169 *Oryza* matches is at the end of a contig, precluding prediction of a fold-back structure.
[b]As with *Arabidopsis,* only one of the miR171 *Oryza* matches has a predicted fold-back characteristic of miRNAs.